

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao

(ii) TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related Ligands and Uses Therefor

(iii) NUMBER OF SEQUENCES: 23

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Genentech, Inc.
- (B) STREET: 1 DNA Way
- (C) CITY: South San Francisco
- (D) STATE: California
- (E) COUNTRY: USA
- (F) ZIP: 94080

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: Unassigned
- (B) FILING DATE: 30-Jun-1998
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Conley, Deirdre L.
- (B) REGISTRATION NUMBER: 36,487
- (C) REFERENCE/DOCKET NUMBER: P1084R1-1

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 650/225-2066
- (B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2538 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: mouse NRG3 nucleic acid
- (B) LOCATION: 1-2538
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

GAATGCTTTG TGATTGAGAC CCTGACAGGA TCCCATAAGC ACTGTCGGTG 1250
CAAGGAAGGC TACCAAGGAG TCCGTTGTGA TCAATTTCTG CCGAAAACAG 1300
ACTCCATCTT ATCGGATCCA ACAGACCACT TGGGGATTGA ATTCATGGAG 1350
AGTGAAGACG TTTATCAAAG GCAGGTGCTG TCAATTTTCAT GTATCATCTT 1400
TGGAATTGTC ATCGTGGGCA TGTTCGTGTC AGCATTCTAC TTCAAAAGCA 1450
AGAAACAAGC TAAACAAATT CAGGAGCACC TGAAAGAGTC ACAGAATGGG 1500
AAGAACTACA GCCTCAAGGC ATCCAGCACA AAGTCTGAGA GCTTGATGAA 1550
GAGCCATGTC CATCTACAAA ATTATTCAAA GGCGGATAGG CATCCTGTGA 1600
CTGCGCTGGA GAAAATAATG GAGTCAAGTT TTTCAGCTCC CCAGTCGTTT 1650
CCAGAAGTCA CTTCTCCTGA CCGAGGAAGC CAGCCTATCA AGCACCACAG 1700
CCCAGGACAA AGGAGTGGGA TGTTGCATAG GAATACTTTC AGAAGGGCAC 1750
CACCCCTCACC CCGAAGTCGA CTGGGTGGTA TTGTAGGACC AGCATATCAA 1800
CAACTTGAAG AATCAAGAAT TCCAGACCAG GATACGATAC CTTGCCAAGG 1850
GATAGAGGTC AGGAAGACTA TATCCCACCT GCCTATACAG CTGTGGTGTG 1900
TTGAAAGACC CCTGGACTTA AAGTATGTGT CCAATGGCTT AAGAACCCAA 1950
CAAATGCAT CAATAAATAT GCAACTGCCT TCAAGAGAGA CAAACCCCTA 2000
TTTTAATAGC TTGGATCAAA AGGACCTGGT GGGTTATTTA TCCCCAAGGG 2050
CCAATTCTGT GCCCATCATC CCGTCGATGG GTCTAGAAGA AACCTGCATG 2100
CAAATGCCAG GGATTTCTGA CGTCAAAAGC ATTAAATGGT GCAAAAACCTC 2150
CTACTCCGCT GACATTGTCA ACGCGAGTAT GCCAGTCAGT GATTGTCTTC 2200
TAGAAGAACA ACAGGAAGTG AAAATATTAC TAGAGACTGT GCAGGAACAG 2250
ATCCGGATTC TGACTGATGC CAGACGGTCA GAAGACTTCG AACTGGCCAG 2300
CATGGAAACT GAGGACAGTG CGAGCGAAAA CACAGCCTTT CTCCCCCTGA 2350
GTCCCACGGC CAAATCAGAA CGAGAGGCAC AATTTGTCTT AAGAAATGAA 2400
ATACAAAGAG ACTCTGTGCT AACCAAGTGA CTGGAAATGT AGGAATCTGT 2450
GCATTATATG CTTTGCTAAA CAGGAAGGAG AGGAAATTAA ATACAAATTA 2500

TTTATATGCA TTAATTTAAG AGCATCTACT TAGAAGCC 2538

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 713 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: Mouse NRG3 (mNRG3)/amino acid seq.
- (B) LOCATION: 1-713
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Glu	Gly	Ala	Ala	Gly	Ala	Ser	Pro	Pro	Gly	Ala	Ala	Ser	1	5	10	15
Ala	Ala	Ala	Ala	Ser	Ala	Glu	Glu	Gly	Thr	Ala	Ala	Ala	Ala	Ala	20	25	30	
Ala	Ala	Ala	Ala	Gly	Gly	Gly	Pro	Asp	Gly	Gly	Gly	Glu	Gly	Ala	35	40	45	
Ala	Glu	Pro	Pro	Arg	Glu	Leu	Arg	Cys	Ser	Asp	Cys	Ile	Val	Trp	50	55	60	
Asn	Arg	Gln	Gln	Thr	Trp	Leu	Cys	Val	Val	Pro	Leu	Phe	Ile	Gly	65	70	75	
Phe	Ile	Gly	Leu	Gly	Leu	Ser	Leu	Met	Leu	Leu	Lys	Trp	Ile	Val	80	85	90	
Val	Gly	Ser	Val	Lys	Glu	Tyr	Val	Pro	Thr	Asp	Leu	Val	Asp	Ser	95	100	105	
Lys	Gly	Met	Gly	Gln	Asp	Pro	Phe	Phe	Leu	Ser	Lys	Pro	Ser	Ser	110	115	120	
Phe	Pro	Lys	Ala	Met	Glu	Thr	Thr	Thr	Thr	Thr	Thr	Ser	Thr	Thr	125	130	135	
Ser	Pro	Ala	Thr	Pro	Ser	Ala	Gly	Gly	Ala	Ala	Ser	Ser	Arg	Thr	140	145	150	
Pro	Asn	Arg	Ile	Ser	Thr	Arg	Leu	Thr	Thr	Ile	Thr	Arg	Ala	Pro	155	160	165	
Thr	Arg	Phe	Pro	Gly	His	Arg	Val	Pro	Ile	Arg	Ala	Ser	Pro	Arg	170	175	180	

Ser	Thr	Thr	Ala	Arg	Asn	Thr	Ala	Ala	Pro	Pro	Thr	Val	Leu	Ser	185	190	195
Thr	Thr	Ala	Pro	Phe	Phe	Ser	Ser	Ser	Thr	Pro	Gly	Ser	Arg	Pro	200	205	210
Pro	Met	Pro	Gly	Ala	Pro	Ser	Thr	Gln	Ala	Met	Pro	Ser	Trp	Pro	215	220	225
Thr	Ala	Ala	Tyr	Ala	Thr	Ser	Ser	Tyr	Leu	His	Asp	Ser	Thr	Pro	230	235	240
Ser	Trp	Thr	Leu	Ser	Pro	Phe	Gln	Asp	Ala	Ala	Ala	Ala	Ser	Ser	245	250	255
Ser	Ser	Pro	Ser	Ser	Thr	Ser	Ser	Thr	Thr	Thr	Thr	Pro	Glu	Thr	260	265	270
Ser	Thr	Ser	Pro	Lys	Phe	His	Thr	Thr	Thr	Tyr	Ser	Thr	Glu	Arg	275	280	285
Ser	Glu	His	Phe	Lys	Pro	Cys	Arg	Asp	Lys	Asp	Leu	Ala	Tyr	Cys	290	295	300
Leu	Asn	Asp	Gly	Glu	Cys	Phe	Val	Ile	Glu	Thr	Leu	Thr	Gly	Ser	305	310	315
His	Lys	His	Cys	Arg	Cys	Lys	Glu	Gly	Tyr	Gln	Gly	Val	Arg	Cys	320	325	330
Asp	Gln	Phe	Leu	Pro	Lys	Thr	Asp	Ser	Ile	Leu	Ser	Asp	Pro	Thr	335	340	345
Asp	His	Leu	Gly	Ile	Glu	Phe	Met	Glu	Ser	Glu	Asp	Val	Tyr	Gln	350	355	360
Arg	Gln	Val	Leu	Ser	Ile	Ser	Cys	Ile	Ile	Phe	Gly	Ile	Val	Ile	365	370	375
Val	Gly	Met	Phe	Cys	Ala	Ala	Phe	Tyr	Phe	Lys	Ser	Lys	Lys	Gln	380	385	390
Ala	Lys	Gln	Ile	Gln	Glu	His	Leu	Lys	Glu	Ser	Gln	Asn	Gly	Lys	395	400	405
Asn	Tyr	Ser	Leu	Lys	Ala	Ser	Ser	Thr	Lys	Ser	Glu	Ser	Leu	Met	410	415	420
Lys	Ser	His	Val	His	Leu	Gln	Asn	Tyr	Ser	Lys	Ala	Asp	Arg	His	425	430	435

Pro Val Thr Ala	Leu Glu Lys Ile Met	Glu Ser Ser Phe Ser	Ala
440		445	450
Pro Gln Ser Phe	Pro Glu Val Thr Ser	Pro Asp Arg Gly Ser	Gln
455		460	465
Pro Ile Lys His	His Ser Pro Gly Gln	Arg Ser Gly Met Leu	His
470		475	480
Arg Asn Thr Phe	Arg Arg Ala Pro Pro	Ser Pro Arg Ser Arg	Leu
485		490	495
Gly Gly Ile Val	Gly Pro Ala Tyr Gln	Gln Leu Glu Glu Ser	Arg
500		505	510
Ile Pro Asp Gln	Asp Thr Ile Pro Cys	Gln Gly Ile Glu Val	Arg
515		520	525
Lys Thr Ile Ser	His Leu Pro Ile Gln	Leu Trp Cys Val Glu	Arg
530		535	540
Pro Leu Asp Leu	Lys Tyr Val Ser Asn	Gly Leu Arg Thr Gln	Gln
545		550	555
Asn Ala Ser Ile	Asn Met Gln Leu Pro	Ser Arg Glu Thr Asn	Pro
560		565	570
Tyr Phe Asn Ser	Leu Asp Gln Lys Asp	Leu Val Gly Tyr Leu	Ser
575		580	585
Pro Arg Ala Asn	Ser Val Pro Ile Ile	Pro Ser Met Gly Leu	Glu
590		595	600
Glu Thr Cys Met	Gln Met Pro Gly Ile	Ser Asp Val Lys Ser	Ile
605		610	615
Lys Trp Cys Lys	Asn Ser Tyr Ser Ala	Asp Ile Val Asn Ala	Ser
620		625	630
Met Pro Val Ser	Asp Cys Leu Leu Glu	Glu Gln Gln Glu Val	Lys
635		640	645
Ile Leu Leu Glu	Thr Val Gln Glu Gln	Ile Arg Ile Leu Thr	Asp
650		655	660
Ala Arg Arg Ser	Glu Asp Phe Glu Leu	Ala Ser Met Glu Thr	Glu
665		670	675
Asp Ser Ala Ser	Glu Asn Thr Ala Phe	Leu Pro Leu Ser Pro	Thr
680		685	690

	155		160		165
Thr Arg Phe Pro Gly His Arg Val Pro Ile Arg Ala Ser Pro Arg	170		175		180
Ser Thr Thr Ala Arg Asn Thr Ala Ala Pro Pro Thr Val Leu Ser	185		190		195
Thr Thr Ala Pro Phe Phe Ser Ser Ser Thr Pro Gly Ser Arg Pro	200		205		210
Pro Met Pro Gly Ala Pro Ser Thr Gln Ala Met Pro Ser Trp Pro	215		220		225
Thr Ala Ala Tyr Ala Thr Ser Ser Tyr Leu His Asp Ser Thr Pro	230		235		240
Ser Trp Thr Leu Ser Pro Phe Gln Asp Ala Ala Ala Ala Ser Ser	245		250		255
Ser Ser Pro Ser Ser Thr Ser Ser Thr Thr Thr Thr Pro Glu Thr	260		265		270
Ser Thr Ser Pro Lys Phe His Thr Thr Thr Tyr Ser Thr Glu Arg	275		280		285
Ser Glu His Phe Lys Pro Cys Arg Asp Lys Asp Leu Ala Tyr Cys	290		295		300
Leu Asn Asp Gly Glu Cys Phe Val Ile Glu Thr Leu Thr Gly Ser	305		310		315
His Lys His Cys Arg Cys Lys Glu Gly Tyr Gln Gly Val Arg Cys	320		325		330
Asp Gln Phe Leu Pro Lys Thr Asp Ser Ile Leu Ser Asp Pro Thr	335		340		345
Asp His Leu Gly Ile Glu Phe Met Glu Ser Glu Asp Val Tyr Gln	350		355		360
Arg Gln	362				

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 47 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

09876-0000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

(2) INFORMATION FOR SEQ ID NO:5:

(ix) FEATURE:

(A) NAME/KEY: Human NRG3B1(hNRG3B1)/nucleic acid seq.
(B) LOCATION: 1-2502
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

102

CAAATGGATC GTGGTGGGCT CCGTCAAGGA GTACGTGCCC ACCGACCTAG 450
TGGACTCCAA GGGGATGGGC CAGGACCCCT TCTTCCTCTC CAAGCCCAGC 500
TCTTTCCCCA AGGCCATGGA GACCACCACC ACTACCACTT CCACCACGTC 550
CCCCGCCACC CCCTCCGCCG GGGGTGCCGC CTCCTCCAGG ACGCCCAACC 600
GGATTAGCAC TCGCCTGACC ACCATCACGC GGGCGCCCAC TCGCTTCCCC 650
GGGCACCGGG TGCCCATCCG GGCCAGCCCG CGCTCCACCA CAGCACGGAA 700
CACTGCGGCC CCTGCGACGG TCCCGTCCAC CACGGCCCCG TTCTTCAGTA 750
GCAGCACGCT GGGCTCCCGA CCCCCGGTGC CAGGAACTCC AAGTACCCAG 800
GCAATGCCCT CCTGGCCTAC TGCGGCATAC GCTACCTCCT CCTACCTTCA 850
CGATTCTACT CCCTCCTGGA CCCTGTCTCC CTTTCAGGAT GCTGCCTCCT 900
CTTCTTCCTC TTCTTCCTCC TCCGCTACCA CCACCACACC AGAAACTAGC 950
ACCAGCCCCA AATTCATAC GACGACATAT TCCACAGAGC GATCCGAGCA 1000
CTTCAAACCC TGCCGAGACA AGGACCTTGC ATACTGTCTC AATGATGGCG 1050
AGTGCTTTGT GATCGAAACC CTGACCGGAT CCCATAAACA CTGTCGGTGC 1100
AAAGAAGGCT ACCAAGGAGT CCGTTGTGAT CAATTTCTGC CGAAAACCTGA 1150
TTCCATCTTA TCGGATCCAA CAGACCACTT GGGGATTGAA TTCATGGAGA 1200
GTGAAGAAGT TTATCAAAGG CAGGTGCTGT CAATTTCATG TATCATCTTT 1250
GGAATTGTCA TCGTGGGCAT GTTCTGTGCA GCATTCTACT TCAAAAGCAA 1300
GAAACAAGCT AAACAAATCC AAGAGCAGCT GAAAGTGCCA CAAAATGGTA 1350
AAAGCTACAG TCTCAAAGCA TCCAGCACAA TGGCAAAGTC AGAGAACTTG 1400
GTGAAGAGCC ATGTCCAGCT GCAAAATTAT TCAAAGGTGG AAAGGCATCC 1450
TGTGACTGCA TTGGAGAAAA TGATGGAGTC AAGTTTTGTC GGCCCCCAGT 1500
CATTCCCTGA GGTCCCTTCT CCTGACAGAG GAAGCCAGTC TGTCAAACAC 1550
CACAGGAGTC TATCCTCTTG CTGCAGCCCA GGGCAAAGAA GTGGCATGCT 1600
CCATAGGAAT GCCTTCAGAA GGACACCCCC GTCACCCCGA AGTAGGCTAG 1650
GTGGAATTGT GGGACCAGCA TATCAGCAAC TCGAAGAATC AAGGATCCCA 1700

GACCAGGATA CGATACCTTG CCAAGGGATA GAGGTCAGGA AGACTATATC 1750
 CCACCTGCCT ATACAGCTGT GGTGTGTTGA AAGACCCCTG GACTTAAAGT 1800
 ATTCATCCAG TGGTTTAAAA ACCCAACGAA ATACATCAAT AAATATGCAA 1850
 CTGCCTTCAA GAGAGACAAA CCCCTATTTT AATAGCTTGG AGCAAAAGGA 1900
 CCTGGTGGGC TATTCATCCA CAAGGGCCAG TTCTGTGCCC ATCATCCCTT 1950
 CAGTGGGTTT AGAGGAAACC TGCCTGCAAA TGCCAGGGAT TTCTGAAGTC 2000
 AAAAGCATCA AATGGTGCAA AAACCTCTAT TCAGCTGACG TTGTCAATGT 2050
 GAGTATTCCA GTCAGCGATT GTCTTATAGC AGAACAACAA GAAGTGAAAA 2100
 TATTGCTAGA AACTGTCCAG GAGCAGATCC GAATTCTGAC TGATGCCAGA 2150
 CGGTCAGAAG ACTACGAACT GGCCAGCGTA GAAACCGAGG ACAGTGCAAG 2200
 CGAAAACACA GCCTTTCTCC CCCTGAGTCC CACAGCCAAA TCAGAACGAG 2250
 AGGCGCAATT TGTCTTAAGA AATGAAATAC AAAGAGACTC TGCATTGACC 2300
 AAGTGACTION AGATGTAGGA ATCTGTGCAT TCTATGCTTT GCTCAACAGG 2350
 AAAGAGAGGA AATCAAATAC AAATTATTTA TATGCATTAA TTTAAGAGCA 2400
 TCTACTTAGA AGAAACCAAA TAGTCTATCG CCCTCATATC ATAGTGTTTT 2450
 TTAACAAAAT ATTTTTTTAA GGGAAAGAAA TGTTTCAGGA GGGATAAAGC 2500
 TT 2502

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hNRG3B1 amino acid sequence
- (B) LOCATION: 1-720
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Ser	Glu	Gly	Ala	Ala	Ala	Ala	Ser	Pro	Pro	Gly	Ala	Ala	Ser
1				5					10					15

Ala	Ala	Ala	Ala	Ser	Ala	Glu	Glu	Gly	Thr	Ala	Ala	Ala	Ala	Ala	20	25	30
Ala	Ala	Ala	Ala	Gly	Gly	Gly	Pro	Asp	Gly	Gly	Gly	Glu	Gly	Ala	35	40	45
Ala	Glu	Pro	Pro	Arg	Glu	Leu	Arg	Cys	Ser	Asp	Cys	Ile	Val	Trp	50	55	60
Asn	Arg	Gln	Gln	Thr	Trp	Leu	Cys	Val	Val	Pro	Leu	Phe	Ile	Gly	65	70	75
Phe	Ile	Gly	Leu	Gly	Leu	Ser	Leu	Met	Leu	Leu	Lys	Trp	Ile	Val	80	85	90
Val	Gly	Ser	Val	Lys	Glu	Tyr	Val	Pro	Thr	Asp	Leu	Val	Asp	Ser	95	100	105
Lys	Gly	Met	Gly	Gln	Asp	Pro	Phe	Phe	Leu	Ser	Lys	Pro	Ser	Ser	110	115	120
Phe	Pro	Lys	Ala	Met	Glu	Thr	Thr	Thr	Thr	Thr	Thr	Ser	Thr	Thr	125	130	135
Ser	Pro	Ala	Thr	Pro	Ser	Ala	Gly	Gly	Ala	Ala	Ser	Ser	Arg	Thr	140	145	150
Pro	Asn	Arg	Ile	Ser	Thr	Arg	Leu	Thr	Thr	Ile	Thr	Arg	Ala	Pro	155	160	165
Thr	Arg	Phe	Pro	Gly	His	Arg	Val	Pro	Ile	Arg	Ala	Ser	Pro	Arg	170	175	180
Ser	Thr	Thr	Ala	Arg	Asn	Thr	Ala	Ala	Pro	Ala	Thr	Val	Pro	Ser	185	190	195
Thr	Thr	Ala	Pro	Phe	Phe	Ser	Ser	Ser	Thr	Leu	Gly	Ser	Arg	Pro	200	205	210
Pro	Val	Pro	Gly	Thr	Pro	Ser	Thr	Gln	Ala	Met	Pro	Ser	Trp	Pro	215	220	225
Thr	Ala	Ala	Tyr	Ala	Thr	Ser	Ser	Tyr	Leu	His	Asp	Ser	Thr	Pro	230	235	240
Ser	Trp	Thr	Leu	Ser	Pro	Phe	Gln	Asp	Ala	Ala	Ser	Ser	Ser	Ser	245	250	255
Ser	Ser	Ser	Ser	Ser	Ala	Thr	Thr	Thr	Thr	Pro	Glu	Thr	Ser	Thr	260	265	270

Ser	Pro	Lys	Phe	His	Thr	Thr	Thr	Tyr	Ser	Thr	Glu	Arg	Ser	Glu	275	280	285
His	Phe	Lys	Pro	Cys	Arg	Asp	Lys	Asp	Leu	Ala	Tyr	Cys	Leu	Asn	290	295	300
Asp	Gly	Glu	Cys	Phe	Val	Ile	Glu	Thr	Leu	Thr	Gly	Ser	His	Lys	305	310	315
His	Cys	Arg	Cys	Lys	Glu	Gly	Tyr	Gln	Gly	Val	Arg	Cys	Asp	Gln	320	325	330
Phe	Leu	Pro	Lys	Thr	Asp	Ser	Ile	Leu	Ser	Asp	Pro	Thr	Asp	His	335	340	345
Leu	Gly	Ile	Glu	Phe	Met	Glu	Ser	Glu	Glu	Val	Tyr	Gln	Arg	Gln	350	355	360
Val	Leu	Ser	Ile	Ser	Cys	Ile	Ile	Phe	Gly	Ile	Val	Ile	Val	Gly	365	370	375
Met	Phe	Cys	Ala	Ala	Phe	Tyr	Phe	Lys	Ser	Lys	Lys	Gln	Ala	Lys	380	385	390
Gln	Ile	Gln	Glu	Gln	Leu	Lys	Val	Pro	Gln	Asn	Gly	Lys	Ser	Tyr	395	400	405
Ser	Leu	Lys	Ala	Ser	Ser	Thr	Met	Ala	Lys	Ser	Glu	Asn	Leu	Val	410	415	420
Lys	Ser	His	Val	Gln	Leu	Gln	Asn	Tyr	Ser	Lys	Val	Glu	Arg	His	425	430	435
Pro	Val	Thr	Ala	Leu	Glu	Lys	Met	Met	Glu	Ser	Ser	Phe	Val	Gly	440	445	450
Pro	Gln	Ser	Phe	Pro	Glu	Val	Pro	Ser	Pro	Asp	Arg	Gly	Ser	Gln	455	460	465
Ser	Val	Lys	His	His	Arg	Ser	Leu	Ser	Ser	Cys	Cys	Ser	Pro	Gly	470	475	480
Gln	Arg	Ser	Gly	Met	Leu	His	Arg	Asn	Ala	Phe	Arg	Arg	Thr	Pro	485	490	495
Pro	Ser	Pro	Arg	Ser	Arg	Leu	Gly	Gly	Ile	Val	Gly	Pro	Ala	Tyr	500	505	510
Gln	Gln	Leu	Glu	Glu	Ser	Arg	Ile	Pro	Asp	Gln	Asp	Thr	Ile	Pro	515	520	525

Cys	Gln	Gly	Ile	Glu	Val	Arg	Lys	Thr	Ile	Ser	His	Leu	Pro	Ile	530	535	540
Gln	Leu	Trp	Cys	Val	Glu	Arg	Pro	Leu	Asp	Leu	Lys	Tyr	Ser	Ser	545	550	555
Ser	Gly	Leu	Lys	Thr	Gln	Arg	Asn	Thr	Ser	Ile	Asn	Met	Gln	Leu	560	565	570
Pro	Ser	Arg	Glu	Thr	Asn	Pro	Tyr	Phe	Asn	Ser	Leu	Glu	Gln	Lys	575	580	585
Asp	Leu	Val	Gly	Tyr	Ser	Ser	Thr	Arg	Ala	Ser	Ser	Val	Pro	Ile	590	595	600
Ile	Pro	Ser	Val	Gly	Leu	Glu	Glu	Thr	Cys	Leu	Gln	Met	Pro	Gly	605	610	615
Ile	Ser	Glu	Val	Lys	Ser	Ile	Lys	Trp	Cys	Lys	Asn	Ser	Tyr	Ser	620	625	630
Ala	Asp	Val	Val	Asn	Val	Ser	Ile	Pro	Val	Ser	Asp	Cys	Leu	Ile	635	640	645
Ala	Glu	Gln	Gln	Glu	Val	Lys	Ile	Leu	Leu	Glu	Thr	Val	Gln	Glu	650	655	660
Gln	Ile	Arg	Ile	Leu	Thr	Asp	Ala	Arg	Arg	Ser	Glu	Asp	Tyr	Glu	665	670	675
Leu	Ala	Ser	Val	Glu	Thr	Glu	Asp	Ser	Ala	Ser	Glu	Asn	Thr	Ala	680	685	690
Phe	Leu	Pro	Leu	Ser	Pro	Thr	Ala	Lys	Ser	Glu	Arg	Glu	Ala	Gln	695	700	705
Phe	Val	Leu	Arg	Asn	Glu	Ile	Gln	Arg	Asp	Ser	Ala	Leu	Thr	Lys	710	715	720

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hNRG3 extracellular domain/Amino AcidSeq
- (B) LOCATION: 1-360
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Ser	Glu	Gly	Ala	Ala	Ala	Ala	Ser	Pro	Pro	Gly	Ala	Ala	Ser	
1				5					10					15	
Ala	Ala	Ala	Ala	Ser	Ala	Glu	Glu	Gly	Thr	Ala	Ala	Ala	Ala	Ala	
				20					25					30	
Ala	Ala	Ala	Ala	Gly	Gly	Gly	Pro	Asp	Gly	Gly	Gly	Glu	Gly	Ala	
				35					40					45	
Ala	Glu	Pro	Pro	Arg	Glu	Leu	Arg	Cys	Ser	Asp	Cys	Ile	Val	Trp	
				50					55					60	
Asn	Arg	Gln	Gln	Thr	Trp	Leu	Cys	Val	Val	Pro	Leu	Phe	Ile	Gly	
				65					70					75	
Phe	Ile	Gly	Leu	Gly	Leu	Ser	Leu	Met	Leu	Leu	Lys	Trp	Ile	Val	
				80					85					90	
Val	Gly	Ser	Val	Lys	Glu	Tyr	Val	Pro	Thr	Asp	Leu	Val	Asp	Ser	
				95					100					105	
Lys	Gly	Met	Gly	Gln	Asp	Pro	Phe	Phe	Leu	Ser	Lys	Pro	Ser	Ser	
				110					115					120	
Phe	Pro	Lys	Ala	Met	Glu	Thr	Thr	Thr	Thr	Thr	Thr	Ser	Thr	Thr	
				125					130					135	
Ser	Pro	Ala	Thr	Pro	Ser	Ala	Gly	Gly	Ala	Ala	Ser	Ser	Arg	Thr	
				140					145					150	
Pro	Asn	Arg	Ile	Ser	Thr	Arg	Leu	Thr	Thr	Ile	Thr	Arg	Ala	Pro	
				155					160					165	
Thr	Arg	Phe	Pro	Gly	His	Arg	Val	Pro	Ile	Arg	Ala	Ser	Pro	Arg	
				170					175					180	
Ser	Thr	Thr	Ala	Arg	Asn	Thr	Ala	Ala	Pro	Ala	Thr	Val	Pro	Ser	
				185					190					195	
Thr	Thr	Ala	Pro	Phe	Phe	Ser	Ser	Ser	Thr	Leu	Gly	Ser	Arg	Pro	
				200					205					210	
Pro	Val	Pro	Gly	Thr	Pro	Ser	Thr	Gln	Ala	Met	Pro	Ser	Trp	Pro	
				215					220					225	
Thr	Ala	Ala	Tyr	Ala	Thr	Ser	Ser	Tyr	Leu	His	Asp	Ser	Thr	Pro	
				230					235					240	
Ser	Trp	Thr	Leu	Ser	Pro	Phe	Gln	Asp	Ala	Ala	Ser	Ser	Ser	Ser	
				245					250					255	

Ser	Ser	Ser	Ser	Ser	Ala	Thr	Thr	Thr	Thr	Pro	Glu	Thr	Ser	Thr
				260						265				270
Ser	Pro	Lys	Phe	His	Thr	Thr	Thr	Tyr	Ser	Thr	Glu	Arg	Ser	Glu
				275					280					285
His	Phe	Lys	Pro	Cys	Arg	Asp	Lys	Asp	Leu	Ala	Tyr	Cys	Leu	Asn
				290					295					300
Asp	Gly	Glu	Cys	Phe	Val	Ile	Glu	Thr	Leu	Thr	Gly	Ser	His	Lys
				305					310					315
His	Cys	Arg	Cys	Lys	Glu	Gly	Tyr	Gln	Gly	Val	Arg	Cys	Asp	Gln
				320					325					330
Phe	Leu	Pro	Lys	Thr	Asp	Ser	Ile	Leu	Ser	Asp	Pro	Thr	Asp	His
				335					340					345
Leu	Gly	Ile	Glu	Phe	Met	Glu	Ser	Glu	Glu	Val	Tyr	Gln	Arg	Gln
				350					355					360

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: NRG3 EGF-like domain/amino acid seq.
- (B) LOCATION: 1-47
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

His	Phe	Lys	Pro	Cys	Arg	Asp	Lys	Asp	Leu	Ala	Tyr	Cys	Leu	Asn
1				5					10					15
Asp	Gly	Glu	Cys	Phe	Val	Ile	Glu	Thr	Leu	Thr	Gly	Ser	His	Lys
				20					25					30
His	Cys	Arg	Cys	Lys	Glu	Gly	Tyr	Gln	Gly	Val	Arg	Cys	Asp	Gln
				35					40					45
Phe	Leu													
	47													

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: cARIA.egf
(B) LOCATION: 1-48
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

His Leu Thr Lys Cys Asp Ile Lys Gln Lys Ala Phe Cys Val Asn
1 5 10 15
Gly Gly Glu Cys Tyr Met Val Lys Asp Leu Pro Asn Pro Pro Arg
20 25 30
Tyr Leu Cys Arg Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln
35 40 45
Asn Tyr Val
48

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hAR.egf
(B) LOCATION: 1-45
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Lys Lys Asn Pro Cys Asn Ala Glu Phe Gln Asn Phe Cys Ile His
1 5 10 15
Gly Glu Cys Lys Tyr Ile Glu His Leu Glu Ala Val Thr Cys Lys
20 25 30
Cys Gln Gln Glu Tyr Phe Gly Glu Arg Cys Gly Glu Lys Ser Met
35 40 45

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hBTC.efg
(B) LOCATION: 1-45
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

His Phe Ser Arg Cys Pro Lys Gln Tyr Lys His Tyr Cys Ile Lys
1 5 10 15
Gly Arg Cys Arg Phe Val Val Ala Glu Gln Thr Pro Ser Cys Val
20 25 30
Cys Asp Glu Gly Tyr Ile Gly Ala Arg Cys Glu Arg Val Asp Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hEGF.egf
(B) LOCATION: 1-46
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His
1 5 10 15
Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys
20 25 30
Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp
35 40 45
Leu
46

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

- (ix) FEATURE:
(A) NAME/KEY: hHB-EGF.egf
(B) LOCATION: 1-45
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Lys Arg Asp Pro Cys Leu Arg Lys Tyr Lys Asp Phe Cys Ile His
1 5 10 15
Gly Glu Cys Lys Tyr Val Lys Glu Leu Arg Ala Pro Ser Cys Ile
20 25 30
Cys His Pro Gly Tyr His Gly Glu Arg Cys His Gly Leu Ser Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

- (ix) FEATURE:
(A) NAME/KEY: hHRGalpha.egf
(B) LOCATION: 1-49
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1 5 10 15
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg
20 25 30
Tyr Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr
35 40 45
Glu Asn Tyr Pro
49

0967-866X(199609)14:3<251::AID-JCCE251>3.0.CO;2-I

(A) LENGTH: 48 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(A) NAME/KEY: hHRGbeta.egf
(B) LOCATION: 1-48
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

[illegible]

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(A) NAME/KEY: hTGFalpha.egf
(B) LOCATION: 1-45
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

His 1	Phe	Asn	Asp	Cys 5	Pro	Asp	Ser	His	Thr 10	Gln	Phe	Cys	Phe	His 15
Gly	Thr	Cys	Arg	Phe 20	Leu	Val	Gln	Glu	Asp 25	Lys	Pro	Ala	Cys	Val 30
Cys	His	Ser	Gly	Tyr 35	Val	Gly	Ala	Arg	Cys 40	Glu	His	Ala	Asp	Leu 45

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: mEPR.egf
(B) LOCATION: 1-45
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Gln Ile Thr Lys Cys Ser Ser Asp Met Asp Gly Tyr Cys Leu His
1 5 10 15
Gly Gln Cys Ile Tyr Leu Val Asp Met Arg Glu Lys Phe Cys Arg
20 25 30
Cys Glu Val Gly Tyr Thr Gly Leu Arg Cys Glu His Phe Phe Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: Oligonucleotide probe
(B) LOCATION: 1-50
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Thr Gly Gly Thr Ala Ala Ala Ala Gly Cys Thr Ala Cys Ala Gly
1 5 10 15
Thr Cys Thr Cys Ala Ala Ala Gly Cys Ala Thr Cys Cys Ala Gly
20 25 30
Cys Ala Cys Ala Ala Thr Gly Gly Cys Ala Ala Ala Gly Thr Cys
35 40 45
Ala Gly Ala Gly Ala
50

090767-1

(A) LENGTH: 8 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(A) NAME/KEY: hNRG3B1 transmembrane proximal 1
(B) LOCATION: 1-8
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

Asn Asp Gly Glu Cys Phe Val Ile
1 5 8

(A) LENGTH: 9 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(A) NAME/KEY: hNRG3B1 transmembrane proximal 2
(B) LOCATION: 1-9
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

Glu Phe Met Glu Ser Glu Glu Val Tyr
1 5 9

(A) LENGTH: 466 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(A) NAME/KEY: EST Genbank entry H23651
(B) LOCATION: 1-466
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AATTTCTGCC GAAAACTGAT TCCATCTTAT CGGATCCAAC AGACCACTTG 50
GGGATTGAAT TCATGGAGAG TGAAGAAGTT TATCAAAGGC AGGTGCTGTC 100
AATTTTCATGT ATCATCTTTG GAATTGTCAT CGTGGGCATG TTCTGTGCAG 150
CATTCTACTT CAAAAGCAAG AAACAAGCTA AACAAATCCA AGAGCAGCTG 200
AAAGTGCCAC AAAATGGTAA AAGCTACAGT CTCAAAGCAT CCAGCACAAT 250
GGCAAAGTCA GAGAACTTGG TGAAGAGCCA TGTCCAGCTG CAAAATAAAA 300
TGTCAGGCTT CTGAGCCCAA GCTAAGCCAT CATATCCCCT GTNGACCTGC 350
ACGTGCACAT CCNGATGGCC CGTTTCCTGC CTTTNTGAT GACATTTNCA 400
CCACAAATGN AGTGAAAATG GGNCTTTTCN TGCCTTAACT GGTGACNTT 450
TTNCCCCAA AAGGAG 466

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2091 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATGAGTGAAG GGGCGGCCGC TGCCTCGCCA CCTGGTGCCG CTCGGCAGC 50
CGCCGCCTCG GCCGAGGAGG GCACCGCGGC GGCTGCGGCG GCGGCAGCGG 100
CGGGCGGGGG CCCGGACGGC GGCGGCGAAG GGGCGGCCGA GCCCCCCC GG 150
GAGTTACGCT GTAGCGACTG CATCGTGTGG AACCGGCAGC AGACGTGGCT 200
GTGCGTGGTA CCTCTGTTCA TCGGCTTCAT CGGCCTGGGG CTCAGCCTCA 250
TGCTTCTCAA ATGGATCGTG GTGGGCTCCG TCAAGGAGTA CGTGCCCACC 300
GACCTAGTGG ACTCCAAGGG GATGGGCCAG GACCCCTTCT TCCTCTCCAA 350
GCCCAGCTCT TTCCCCAAGG CCATGGAGAC CACCACCACT ACCACTTCCA 400
CCACGTCCCC CGCCACCCCC TCCGCCGGGG GTGCCGCCTC CTCCAGGACG 450

CCCAACCGGA TTAGCACTCG CCTGACCACC ATCACGCGGG CGCCCACTCG 500
 CTTCCCCGGG CACCGGGTGC CCATCCGGGC CAGCCCGCGC TCCACCACAG 550
 CACGGAACAC TGCGGCCCCT GCGACGGTCC CGTCCACCAC GGCCCCGTTC 600
 TTCAGTAGCA GCACGCTGGG CTCCCGACCC CCGGTGCCAG GAACTCCAAG 650
 TACCCAGGCA ATGCCCTCCT GGCCTACTGC GGCATACGCT ACCTCCTCCT 700
 ACCTTCACGA TTCTACTCCC TCCTGGACCC TGTCTCCCTT TCAGGATGCT 750
 GCCTCCTCTT CTTCTCTTTC TTCCTCCTCC GCTACCACCA CCACACCAGA 800
 AACTAGCACC AGCCCCAAT TTCATACGAC GACATATTCC ACAGAGCGAT 850
 CCGAGCACTT CAAACCCTGC CGAGACAAGG ACCTTGCATA CTGTCTCAAT 900
 GATGGCGAGT GCTTTGTGAT CGAAACCCTG ACCGGATCCC ATAAACACTG 950
 TCGGTGCAAA GAAGGCTACC AAGGAGTCCG TTGTGATCAA TTTCTGCCGA 1000
 AAAGTATTC CATCTTATCG GATCCAACAG ACCACTTGGG GATTGAATTC 1050
 ATGGAGAGTG AAGAAGTTTA TCAAAGGCAG GTGCTGTCAA TTTCATGTAT 1100
 CATCTTTGGA ATTGTCATCG TGGGCATGTT CTGTGCAGCA TTCTACTTCA 1150
 AAAGCAAGAA ACAAGCTAAA CAAATCCAAG AGCAGCTGAA AGTGCCACAA 1200
 AATGGTAAAA GCTACAGTCT CAAAGCATCC AGCACAATGG CAAAGTCAGA 1250
 GAACTTGGTG AAGAGCCATG TCCAGCTGCA AAATTATTCA AAGGTGGAAA 1300
 GGCATCCTGT GACTGCATTG GAGAAAATGA TGGAGTCAAG TTTTGTCCGC 1350
 CCCCAGTCAT TCCCTGAGGT CCCTTCTCCT GACAGAGGAA GCCAGTCTGT 1400
 CAAACACCAC AGGAGTCTAT CCTCTTGCTG CAGCCCAGGG CAAAGAAGTG 1450
 GCATGCTCCA TAGGAATGCC TTCAGAAGGA CACCCCCGTC ACCCCGAAGT 1500
 AGGCTAGGTG GAATTGTGGG ACCAGCATAT CAGCAACTCG AAGAATCAAG 1550
 GATCCCAGAC CAGGATACGA TACCTTGCCA AGGGTATTCA TCCAGTGGTT 1600
 TAAAAACCCA ACGAAATACA TCAATAAATA TGCAACTGCC TTCAAGAGAG 1650
 ACAAACCCCT ATTTTAATAG CTTGGAGCAA AAGGACCTGG TGGGCTATTC 1700
 ATCCACAAGG GCCAGTTCTG TGCCCATCAT CCCTTCAGTG GGTTTAGAGG 1750

AACCTGCCT GCAAATGCCA GGGATTTCTG AAGTCAAAAG CATCAAATGG 1800
 TGCAAAAACCT CCTATTCAGC TGACGTTGTC AATGTGAGTA TTCCAGTCAG 1850
 CGATTGTCTT ATAGCAGAAC AACAAGAAGT GAAAATATTG CTAGAAACTG 1900
 TCCAGGAGCA GATCCGAATT CTGACTGATG CCAGACGGTC AGAAGACTAC 1950
 GAACTGGCCA GCGTAGAAAC CGAGGACAGT GCAAGCGAAA ACACAGCCTT 2000
 TCTCCCCCTG AGTCCCACAG CCAAATCAGA ACGAGAGGCG CAATTTGTCT 2050
 TAAGAAATGA AATACAAAGA GACTCTGCAT TGACCAAGTG A 2091

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 696 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: Human NRG3B2
- (B) LOCATION: 1-696
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met	Ser	Glu	Gly	Ala	Ala	Ala	Ala	Ser	Pro	Pro	Gly	Ala	Ala	Ser	1	5	10	15
Ala	Ala	Ala	Ala	Ser	Ala	Glu	Glu	Gly	Thr	Ala	Ala	Ala	Ala	Ala	20	25	30	
Ala	Ala	Ala	Ala	Gly	Gly	Gly	Pro	Asp	Gly	Gly	Gly	Glu	Gly	Ala	35	40	45	
Ala	Glu	Pro	Pro	Arg	Glu	Leu	Arg	Cys	Ser	Asp	Cys	Ile	Val	Trp	50	55	60	
Asn	Arg	Gln	Gln	Thr	Trp	Leu	Cys	Val	Val	Pro	Leu	Phe	Ile	Gly	65	70	75	
Phe	Ile	Gly	Leu	Gly	Leu	Ser	Leu	Met	Leu	Leu	Lys	Trp	Ile	Val	80	85	90	
Val	Gly	Ser	Val	Lys	Glu	Tyr	Val	Pro	Thr	Asp	Leu	Val	Asp	Ser	95	100	105	
Lys	Gly	Met	Gly	Gln	Asp	Pro	Phe	Phe	Leu	Ser	Lys	Pro	Ser	Ser	110	115	120	

09846-0801

0907665-050304

Met	Phe	Cys	Ala	Ala	Phe	Tyr	Phe	Lys	Ser	Lys	Lys	Gln	Ala	Lys	
				380					385					390	
Gln	Ile	Gln	Glu	Gln	Leu	Lys	Val	Pro	Gln	Asn	Gly	Lys	Ser	Tyr	
				395					400					405	
Ser	Leu	Lys	Ala	Ser	Ser	Thr	Met	Ala	Lys	Ser	Glu	Asn	Leu	Val	
				410					415					420	
Lys	Ser	His	Val	Gln	Leu	Gln	Asn	Tyr	Ser	Lys	Val	Glu	Arg	His	
				425					430					435	
Pro	Val	Thr	Ala	Leu	Glu	Lys	Met	Met	Glu	Ser	Ser	Phe	Val	Gly	
				440					445					450	
Pro	Gln	Ser	Phe	Pro	Glu	Val	Pro	Ser	Pro	Asp	Arg	Gly	Ser	Gln	
				455					460					465	
Ser	Val	Lys	His	His	Arg	Ser	Leu	Ser	Ser	Cys	Cys	Ser	Pro	Gly	
				470					475					480	
Gln	Arg	Ser	Gly	Met	Leu	His	Arg	Asn	Ala	Phe	Arg	Arg	Thr	Pro	
				485					490					495	
Pro	Ser	Pro	Arg	Ser	Arg	Leu	Gly	Gly	Ile	Val	Gly	Pro	Ala	Tyr	
				500					505					510	
Gln	Gln	Leu	Glu	Glu	Ser	Arg	Ile	Pro	Asp	Gln	Asp	Thr	Ile	Pro	
				515					520					525	
Cys	Gln	Gly	Tyr	Ser	Ser	Ser	Gly	Leu	Lys	Thr	Gln	Arg	Asn	Thr	
				530					535					540	
Ser	Ile	Asn	Met	Gln	Leu	Pro	Ser	Arg	Glu	Thr	Asn	Pro	Tyr	Phe	
				545					550					555	
Asn	Ser	Leu	Glu	Gln	Lys	Asp	Leu	Val	Gly	Tyr	Ser	Ser	Thr	Arg	
				560					565					570	
Ala	Ser	Ser	Val	Pro	Ile	Ile	Pro	Ser	Val	Gly	Leu	Glu	Glu	Thr	
				575					580					585	
Cys	Leu	Gln	Met	Pro	Gly	Ile	Ser	Glu	Val	Lys	Ser	Ile	Lys	Trp	
				590					595					600	
Cys	Lys	Asn	Ser	Tyr	Ser	Ala	Asp	Val	Val	Asn	Val	Ser	Ile	Pro	
				605					610					615	
Val	Ser	Asp	Cys	Leu	Ile	Ala	Glu	Gln	Gln	Glu	Val	Lys	Ile	Leu	
				620					625					630	

SECRET